crit Bi volumes of 60.1 and 89.0 Å<sup>3</sup> respectively, and accessible surface areas of 75 and 115 Å<sup>2</sup> respectively. This suggests that the relative small size of amino acid 18 in this peptide facilitates interactions with IL-11. However, Gly and Ser differ in their hydrophilicity, suggesting that several factors may interact to govern the suitability of particular amino acid substitutions at position 18 in these peptides. Thus, although IL-11 binding peptides exist which have the amino acid sequence: Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser Val Pro xxx Tyr Pro (SEQ ID No. 9), where xxx is a suitable amino acid, it will be necessary to screen potential IL-11 binding peptides having this sequence using the TRAP assay and/or the bone nodule formation assay in order to determine if they are IL-11 binding peptides.

The replacement paragraphs and tables presented above incorporate changes as indicated by the marked-up versions below.

Additionally, SEQ-ID-NO. 6 depicts the amino acid sequence of an IL-11 binding region identified within the human IL-11R, namely: Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro. The corresponding murine sequence is depicted in SEQ-ID-NO. 8 and is: Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser Val Pro Ser Tyr Pro. These sequences differ in their eighteenth amino acid whereby the human peptide has Gly and the murine sequence has Ser. Gly and Ser are both relatively small amino acid residues, having volumes of 60.1 and 89.0 ų respectively, and accessible surface areas of 75 and 115 Ų respectively. This suggests that the relative small size of amino acid 18 in this peptide facilitates interactions with IL-11. However, Gly and Ser differ in their hydrophilicity, suggesting that several factors may interact to govern the suitability of particular amino acid substitutions at position 18 in these peptides. Thus, although IL-11 binding peptides exist which have the amino acid sequence: Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser Val Pro xxx Tyr Pro (SEQ ID No. 9), where xxx is a suitable amino acid, it will be necessary to screen potential IL-11 binding peptides having this sequence using the TRAP assay and/or the bone nodule formation assay in order to determine if they are IL-11 binding peptides.

In the claims: